

BLAST comparison of coding sequence for attractin (5' untranslated region and 3' untranslated region removed).

Reference sequence: human membrane attractin (long 5' end)

Identity to itself:

Homo sapiens attractin (ATRN), transcript variant 1, mRNA, Length = 8645

Score = 8504 bits (4290), Expect = 0.0

Identities = 4290/4290 (100%)

Strand = Plus / Plus

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Query: 1      atggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcgggcgacggca 60
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Sbjct: 80      atggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcgggcgacggca 139

Query: 61      gcgctcgcgggcaggagcggcgggccgcactgggactgggacgtgaccagggctgggagg 120
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Sbjct: 140     gcgctcgcgggcaggagcggcgggccgcactgggactgggacgtgaccagggctgggagg 199

Query: 121     ccggggctgggggcccgggctgcgcctcccgcggctgctgtctccaccgctgcggccacgg 180
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Sbjct: 200     ccggggctgggggcccgggctgcgcctcccgcggctgctgtctccaccgctgcggccacgg 259

Query: 181     ctgctgctgctgctgttggtgctctcgcgcgcgctgctgctgctgctgctgccctgtgag 240
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Sbjct: 260     ctgctgctgctgctgttggtgctctcgcgcgcgctgctgctgctgctgctgccctgtgag 319

Query: 241     gccgaggccgcggcgggcgggcgggcggtgtcgggctcagccgcagccgaggccaaggaa 300
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Query: 301     tgtgaccggccctgtgtcaacggcggtcgctgcaaccctggcaccggccagtgcgtctgc 360
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Sbjct: 380     tgtgaccggccctgtgtcaacggcggtcgctgcaaccctggcaccggccagtgcgtctgc 439

Query: 361     cccgccggctgggtgggagcaatgccagcactgcgggggcccgttcagactaactgga 420
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Sbjct: 440     cccgccggctgggtgggagcaatgccagcactgcgggggcccgttcagactaactgga 499

Query: 421     tcttctgggtttgtgacagatggacctggaaattataaatacaaaacgaagtgcacgtgg 480
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Sbjct: 500     tcttctgggtttgtgacagatggacctggaaattataaatacaaaacgaagtgcacgtgg 559

Query: 481     ct cattgaaggacagccaaatagaataatgagacttcgtttcaatcattttgctacagag 540
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Query: 601 gcatttagtggcctcattgttcctgagagagatggcaatgagactgtccctgaggttggt 660  
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Query: 661 gccacatcagggttatgccttgctgcatttttttagtgatgctgcttataatttgactgga 720  
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 Sbjct: 740 gccacatcagggttatgccttgctgcatttttttagtgatgctgcttataatttgactgga 799

Query: 721 tttaatattacttacagttttgatatgtgtccaaataactgctcaggccgaggagagtggt 780  
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 Sbjct: 800 tttaatattacttacagttttgatatgtgtccaaataactgctcaggccgaggagagtggt 859

Query: 781 aagatcagtaatagcagcgatactgttgaaatgtgaatgttctgaaaactggaaaggtgaa 840  
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Query: 841 gcatgtgacattcctcactgtacagacaactgtgggttttcctcatcgaggcatctgcaat 900  
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 Sbjct: 920 gcatgtgacattcctcactgtacagacaactgtgggttttcctcatcgaggcatctgcaat 979

Query: 901 tcaagtgatgtcagaggatgctcctgcttctcagactggcagggctcctggatgttcagtt 960  
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 Sbjct: 980 tcaagtgatgtcagaggatgctcctgcttctcagactggcagggctcctggatgttcagtt 1039

Query: 961 cctgtaccagctaaccagtcattttggactcgagaggaatattctaacttaaagctcccc 1020  
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 Sbjct: 1040 cctgtaccagctaaccagtcattttggactcgagaggaatattctaacttaaagctcccc 1099

Query: 1021 agagcatctcataaaagctgtgggtcaatggaaacattatgtggggtgttgaggatatatg 1080  
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 Sbjct: 1100 agagcatctcataaaagctgtgggtcaatggaaacattatgtggggtgttgaggatatatg 1159

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Query: 1141 ccactaaaccgttctgtgaacaatgtgggtgttagatatgggtcattccttggcattatac 1200  
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Query: 1201 aaggataaaaatttacatgtatggaggaaaaatttgattcaactgggaatgtgaccaatgag 1260  
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Sbjct: 1280 aaggataaaaatttacatgtatggaggaaaaatttgattcaactgggaatgtgaccaatgag 1339

Query: 1261 ttgagagtttttcacattcataatgagtcatgggtgttggtgacccctaaggcaaaggag 1320  
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Sbjct: 1340 ttgagagtttttcacattcataatgagtcatgggtgttggtgacccctaaggcaaaggag 1399

Query: 1321 cagtatgcagtggttgggcactctgcacacattgttacactgaagaatggccgagtggtc 1380  
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Sbjct: 1400 cagtatgcagtggttgggcactctgcacacattgttacactgaagaatggccgagtggtc 1459

Query: 1381 atgctgggtcatctttgggtcactgccctctctatggatatataagcaatgtgcaggaatat 1440  
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Sbjct: 1460 atgctgggtcatctttgggtcactgccctctctatggatatataagcaatgtgcaggaatat 1519

Query: 1441 gatttgggataagaacacatggagtatattacacacccaggggtgcccttgtgcaaggggggt 1500  
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Query: 1501 tacggccatagcagtggtttacgaccataggaccagggccctatacgttcatggtgggtac 1560  
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Sbjct: 1580 tacggccatagcagtggtttacgaccataggaccagggccctatacgttcatggtgggtac 1639

Query: 1561 aaggctttcagtgccaataagtagcgggttgagatgatctctaccgatatgatgtggat 1620  
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Sbjct: 1640 aaggctttcagtgccaataagtagcgggttgagatgatctctaccgatatgatgtggat 1699

Query: 1621 acccagatgtggaccattcttaaggacagccgatttttccggttacttgcacacagctgtg 1680  
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Sbjct: 1700 acccagatgtggaccattcttaaggacagccgatttttccggttacttgcacacagctgtg 1759

Query: 1681 atagtgagtggaaccatgctgggtgttggaggaaacacacacaatgacacatctatgagc 1740  
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Sbjct: 1760 atagtgagtggaaccatgctgggtgttggaggaaacacacacaatgacacatctatgagc 1819

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Sbjct: 1940    |||||  
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Sbjct: 2060    ggacctggtattcggtgtgtgtggaacacagggctcgtctcagtgtatctcgtgggcgctg 2119

Query: 2041    gcaactgatgaacaagaagaaaagttaaaatcagaatgtttttccaaaagaactcttgac 2100  
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Sbjct: 2120    gcaactgatgaacaagaagaaaagttaaaatcagaatgtttttccaaaagaactcttgac 2179

Query: 2101    catgacagatgtgaccagcacacagattgttacagctgcacagccaacaccaatgactgc 2160  
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Sbjct: 2180    catgacagatgtgaccagcacacagattgttacagctgcacagccaacaccaatgactgc 2239

Query: 2161    cactggtgcaatgaccattgtgtgtccccaggaaccacagctgctcagaaggccagatctcc 2220  
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Sbjct: 2240    cactggtgcaatgaccattgtgtgtccccaggaaccacagctgctcagaaggccagatctcc 2299

Query: 2221    atttttaggtatgagaattgccccaggataaccccatgtactactgtaacaagaagacc 2280  
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Sbjct: 2300    atttttaggtatgagaattgccccaggataaccccatgtactactgtaacaagaagacc 2359

Query: 2281    agctgcaggagctgtgccctggaccagaactgccagtgaggagccccggaatcaggagtgc 2340  
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Sbjct: 2360    agctgcaggagctgtgccctggaccagaactgccagtgaggagccccggaatcaggagtgc 2419

Query: 2341    attgccctgcccgaataatctgtggcattggctggcatttggttggaactcatgtttg 2400  
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Sbjct: 2420    attgccctgcccgaataatctgtggcattggctggcatttggttggaactcatgtttg 2479

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Sbjct: 2480    aaaattactactgccaaggagaattatgacaatgctaaattgttctgtaggaaccacaat 2539

Query: 2461    gcccttttggttctcttacaaccagaagaaggtagaatttgctcctaagcagctgcga 2520  
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Sbjct: 2540    gcccttttggttctcttacaaccagaagaaggtagaatttgctcctaagcagctgcga 2599

Query: 2521    ataatgcagtcactctcagagcatgtccaagctcaccttaaccccatgggtcggccttcgg 2580  
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Query: 2581 aagatcaatgtgtcctactggtgctgggaagatatgtccccattttacaaatagtttacta 2640  
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Query: 3181 ccagcttgccaatgcaacggccacagtaaatgcatcaatcagagcatctgtgagaagtgt 3240  
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Query: 3241 gagaacctgaccacaggcaagcactgcgagacctgcatactctggcttctacgggtgatccc 3300  
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Query: 3301 accaatggaggggaaatgtcagccatgcaagtgcaatgggcacgcgtctctgtgcaacacc 3360  
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 Sbjct: 3380 accaatggaggggaaatgtcagccatgcaagtgcaatgggcacgcgtctctgtgcaacacc 3439

Query: 3361 aacacgggcaagtgttctgcaccaccaagggcgtaagggggacgagtgccagctatgt 3420  
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 Sbjct: 3560 attgactatcagttcaccttttagtctatcccaggaagatgatcgctattacacagctatc 3619

Query: 3541 aattttgtggctactcctgacgaacaaaacagggatttggacatgttcatcaatgcctcc 3600  
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Query: 3661 gaagagatgcctgttgtttcaaaaaccaacattaaggagtacaaagatagtttctctaatt 3720  
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Query: 3781 acctggcccatcaaaaattcagattgccttctctcagcacagcaattttatggacctggta 3840  
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Query: 3841 cagttcttcgtgactttcttcagttgtttcctctctttgctcctgggtggctgctgtgggt 3900  
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Query: 3901 tggaagatcaaacaaaagttgttgggcctccagacgtagagagcaacttcttcgagagatg 3960  
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Sbjct: 3980 tggagatcaacaaagttgttgggcctccagacgtagagagcaacttcttcgagagatg 4039

Query: 3961 caacagatggccagccgtccctttgcctctgtaaatgtcgcttggaacagatgaggag 4020  
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Sbjct: 4040 caacagatggccagccgtccctttgcctctgtaaatgtcgcttggaacagatgaggag 4099

Query: 4021 cctcctgatcttattggggggagtataaagactgttcccaaaccattgcactggagccg 4080  
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Sbjct: 4100 cctcctgatcttattggggggagtataaagactgttcccaaaccattgcactggagccg 4159

Query: 4081 tgttttggcaacaaagccgctgtcctctctgtgtttgtgaggctccctcgaggcctgggt 4140  
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Sbjct: 4160 tgttttggcaacaaagccgctgtcctctctgtgtttgtgaggctccctcgaggcctgggt 4219

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Sbjct: 4220 ggcatccctcctcctgggcagtcaggtcttgcctgtggccagcgccctgggtggacatttct 4279

Query: 4201 cagcagatgccgatagtgtacaaggagaagtcaggagccgtgagaaaccggaagcagcag 4260  
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Sbjct: 4280 cagcagatgccgatagtgtacaaggagaagtcaggagccgtgagaaaccggaagcagcag 4339

Query: 4261 cccctgcacagcctgggacctgcatctga 4290  
|||||

Sbjct: 4340 cccctgcacagcctgggacctgcatctga 4369

### Identity to secreted attractin (long 5' end)

Homo sapiens attractin (ATRN), transcript variant 2, mRNA, Length = 4116

Score = 7535 bits (3801), Expect = 0.0

Identities = 3801/3801 (100%)

Strand = Plus / Plus

100% identical base pairs, but 88.6% of length therefore 88.6% identical (?)

Query: 1 atggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcggcgacggca 60  
|||||

Sbjct: 80 atggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcggcgacggca 139

Query: 61 gcgctcgcgggcaggagcggcgggccgcactgggactgggacgtgaccagggctgggagg 120  
|||||

Sbjct: 140 gcgctcgcgggcaggagcggcgggccgcactgggactgggacgtgaccagggctgggagg 199

Query: 121 ccggggctgggggcccgggctgcgcctcccgcggctgctgtctccaccgctgcggccacgg 180  
|||||

Sbjct: 200 ccggggctgggggcccgggctgcgcctcccgcggctgctgtctccaccgctgcggccacgg 259

Query: 181 ctgctgctgctgctgttggtgctctcgccgcccgtgctgctgctgctgctgcccctgtgag 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 260 ctgctgctgctgctgttggtgctctcgccgcccgtgctgctgctgctgctgcccctgtgag 319

Query: 241 gccgaggccgcggcggcgccggcggtgtcgggctcagccgcagccgaggccaaggaa 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 320 gccgaggccgcggcggcgccggcggtgtcgggctcagccgcagccgaggccaaggaa 379

Query: 301 tgtgaccggccctgtgtcaacggcggtcgctgcaaccctggcaccggccagtgcgtctgc 360  
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Query: 361 cccgccggctgggtgggcgagcaatgccagcactgcgggggcccgttcagactaactgga 420  
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 Sbjct: 440 cccgccggctgggtgggcgagcaatgccagcactgcgggggcccgttcagactaactgga 499

Query: 421 tcttctgggtttgtgacagatggacctggaaattataaatacaaaacgaagtgcacgtgg 480  
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Query: 481 ctcatgaaggacagccaaatagaataatgagacttcgtttcaatcattttgctacagag 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 560 ctcatgaaggacagccaaatagaataatgagacttcgtttcaatcattttgctacagag 619

Query: 541 tgtagttgggaccatttatatgtttatgatggggactcaatttatgcaccgctagttgct 600  
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 Sbjct: 620 tgtagttgggaccatttatatgtttatgatggggactcaatttatgcaccgctagttgct 679

Query: 601 gcatttagtggcctcattgttcctgagagagatggcaatgagactgtccctgaggttgtt 660  
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 Sbjct: 3860 acctggcccatcaaaattcag 3880

### Identity to secreted attractin (short 5' end)

Homo sapiens attractin (ATRN), transcript variant 3, mRNA, Length = 3894

Score = 6918 bits (3490), Expect = 0.0  
 Identities = 3490/3490 (100%)  
 Strand = Plus / Plus

100% identical base pairs over first 92 base pairs, then deleted region, then 100% identical over 3490 base pairs; therefore 100% identical over 92+3490 bp = 3582 bp, therefore 83.5% of reference length therefore 83.5% identical (?)

Query: 312 ctgtgtcaacggcggtcgctgcaaccctggcaccggccagtgcgctgccccgccggctg 371  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2029 tgaccattgtgtccccaggaaccacagctgctcagaaggccagatctccatttttaggta 2088

Query: 2232 tgagaattgcccccaaggataacccccatgtactactgtaacaagaagaccagctgcaggag 2291  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2089 tgagaattgcccccaaggataacccccatgtactactgtaacaagaagaccagctgcaggag 2148

Query: 2292 ctgtgccctggaccagaactgccagtgggagccccggaatcaggagtgcattgccctgcc 2351  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2149 ctgtgccctggaccagaactgccagtgggagccccggaatcaggagtgcattgccctgcc 2208

Query: 2352 cgaaaaatatctgtggcattggctggcatttggttggaactcatgtttgaaaattactac 2411  
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 Sbjct: 2209 cgaaaaatatctgtggcattggctggcatttggttggaactcatgtttgaaaattactac 2268

Query: 2412 tgccaaggagaattatgacaatgctaaattgttctgtaggaaccacaatgcccttttggc 2471  
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 Sbjct: 2269 tgccaaggagaattatgacaatgctaaattgttctgtaggaaccacaatgcccttttggc 2328

Query: 2472 ttctcttacaacccagaagaaggtagaatttgtccttaagcagctgccaataatgcagtc 2531  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2329 ttctcttacaacccagaagaaggtagaatttgtccttaagcagctgccaataatgcagtc 2388

Query: 2532 atctcagagcatgtccaagctcaccttaaccccatgggtcggccttcggaagatcaatgt 2591  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2389 atctcagagcatgtccaagctcaccttaaccccatgggtcggccttcggaagatcaatgt 2448

Query: 2592 gtcctactggtgctgggaagatatgtcccatattacaaatagtttactacagtggatgcc 2651  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||



Sbjct: 2449 gtctactggtgctgggaagatatgtccccatttacaaatagtttactacagtggatgcc 2508

Query: 2652 gtctgagcccagtgatgctggattctgtggaatTTTatcagaaccagtgactcggggact 2711  
|||||

Sbjct: 2509 gtctgagcccagtgatgctggattctgtggaatTTTatcagaaccagtgactcggggact 2568

Query: 2712 gaaggctgcaacctgcatcaaccactcaatggtagtgctgtgaaaggcctgcaaacca 2771  
|||||

Sbjct: 2569 gaaggctgcaacctgcatcaaccactcaatggtagtgctgtgaaaggcctgcaaacca 2628

Query: 2772 cagtgcctaagcagtgccggacaccatgtgccttgaggacagcatgtggagattgcaccag 2831  
|||||

Sbjct: 2629 cagtgcctaagcagtgccggacaccatgtgccttgaggacagcatgtggagattgcaccag 2688

Query: 2832 cggcagctctgagtgcattggtgcagcaacatgaagcagtggtggactccaatgccta 2891  
|||||

Sbjct: 2689 cggcagctctgagtgcattggtgcagcaacatgaagcagtggtggactccaatgccta 2748

Query: 2892 tgtggcctccttccctTTTtgccagtgatggaatggatatacgatgagcacctgcccccc 2951  
|||||

Sbjct: 2749 tgtggcctccttccctTTTtgccagtgatggaatggatatacgatgagcacctgcccccc 2808

Query: 2952 tgaaaattgttcaggctactgtacctgtagtcattgcttgaggcaaccaggctgtggctg 3011  
|||||

Sbjct: 2809 tgaaaattgttcaggctactgtacctgtagtcattgcttgaggcaaccaggctgtggctg 2868

Query: 3012 gtgtactgatcccagcaatactggcaaagggaatgcatagagggttcctataaaggacc 3071  
|||||

Sbjct: 2869 gtgtactgatcccagcaatactggcaaagggaatgcatagagggttcctataaaggacc 2928

Query: 3072 agtgaagatgccttcgcaagcccctacaggaaatttctatccacagcccctgctcaattc 3131  
|||||

Sbjct: 2929 agtgaagatgccttcgcaagcccctacaggaaatttctatccacagcccctgctcaattc 2988

Query: 3132 cagcatgtgtctagaggacagcagatacaactgggtctttcattcactgtccagcttgcca 3191  
|||||

Sbjct: 2989 cagcatgtgtctagaggacagcagatacaactgggtctttcattcactgtccagcttgcca 3048

Query: 3192 atgcaacggccacagtaaatgcatcaatcagagcatctgtgagaagtgtgagaacctgac 3251  
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Sbjct: 3049 atgcaacggccacagtaaatgcatcaatcagagcatctgtgagaagtgtgagaacctgac 3108

Query: 3252 cacaggcaagcactgcgagacctgcatatctggcttctacggtgatccaccaatggagg 3311  
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Sbjct: 3109 cacaggcaagcactgcgagacctgcatatctggcttctacggtgatccaccaatggagg 3168

Query: 3312 gaaatgtcagccatgcaagtgcaatgggcacgcgtctctgtgcaacaccaacacgggcaa 3371  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3169 gaaatgtcagccatgcaagtgcaatgggcacgcgtctctgtgcaacaccaacacgggcaa 3228

Query: 3372 gtgcttctgcaccaccaagggcgtcaagggggacgagtgccagctatgtgaggtagaaaa 3431  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3229 gtgcttctgcaccaccaagggcgtcaagggggacgagtgccagctatgtgaggtagaaaa 3288

Query: 3432 tcgataccaaggaaaccctctcagaggaacatgttattatactcttcttattgactatca 3491  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3289 tcgataccaaggaaaccctctcagaggaacatgttattatactcttcttattgactatca 3348

Query: 3492 gttcaccttttagtctatcccaggaagatgatcgctattacacagctatcaattttgaggc 3551  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3349 gttcaccttttagtctatcccaggaagatgatcgctattacacagctatcaattttgaggc 3408

Query: 3552 tactcctgacgaacaaaacagggatttggacatgttcatcaatgcctccaagaatttcaa 3611  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3409 tactcctgacgaacaaaacagggatttggacatgttcatcaatgcctccaagaatttcaa 3468

Query: 3612 cctcaacatcacctgggctgccagtttctcagctggaacccaggctggagaagagatgcc 3671  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3469 cctcaacatcacctgggctgccagtttctcagctggaacccaggctggagaagagatgcc 3528

Query: 3672 tgttggtttcaaaaaccaacattaaggagtacaaagatagtttctctaagagaagtttga 3731  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3529 tgttggtttcaaaaaccaacattaaggagtacaaagatagtttctctaagagaagtttga 3588

Query: 3732 ttttcgcaaccacccaaatatcactttctttgtttatgtcagtaatttcacctggcccat 3791  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3589 ttttcgcaaccacccaaatatcactttctttgtttatgtcagtaatttcacctggcccat 3648

Query: 3792 caaaattcag 3801  
 |||||||||  
 Sbjct: 3649 caaaattcag 3658

Score = 182 bits (92), Expect = 4e-42  
 Identities = 92/92 (100%)  
 Strand = Plus / Plus

Query: 1 atgggtggctgcagcggcggcaactgaggcaaggctgaggaggaggacggcggcgacggca 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 80 atgggtggctgcagcggcggcaactgaggcaaggctgaggaggaggacggcggcgacggca 139

Query: 61 gcgctcgcgggcaggagcgggcgccgactg 92  
 ||||||||||||||||||||||||||||||||  
 Sbjct: 140 gcgctcgcgggcaggagcgggcgccgactg 171

## Identity to membrane attractin (short 5' end)

100% identical base pairs over first 92 base pairs, then deleted region, then 100% identical over 3979 base pairs; therefore 100% identical over 92+3979 bp = 4071 bp, therefore 94.9% of reference length therefore 94.9% identical (?)

sequence not shown

## Identity to kiaa0548/AB011120 coding region

Score = 2617 bits (1361), Expect = 0.0  
 Identities = 1361/1361 (100%)  
 Strand = Plus / Plus

100% identical 1361 base pairs but 31.73% of reference length therefore 31.73% identical.

Query: 3009 atacgatgagcacctgccccctgaaaattgttcaggctactgtacctgtagtcattgct 3068  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1 atacgatgagcacctgccccctgaaaattgttcaggctactgtacctgtagtcattgct 60  
 KIAA0548 protein 1 T M S T C P P E N C S G Y C T C S H C

Query: 3069 tggagcaaccaggctgtggctggtgtactgatcccagcaatactggcaaagggaaatgca 3128  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 61 tggagcaaccaggctgtggctggtgtactgatcccagcaatactggcaaagggaaatgca 120  
 KIAA0548 protein 20 L E Q P G C G W C T D P S N T G K G K C

Query: 3129 tagaggggttcctataaaggaccagtgaagatgccttcgcaagcccctacaggaaatttct 3188  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 121 tagaggggttcctataaaggaccagtgaagatgccttcgcaagcccctacaggaaatttct 180  
 KIAA0548 protein 40 I E G S Y K G P V K M P S Q A P T G N F

Query: 3189 atccacagcccctgctcaattccagcatgtgtctagaggacagcagatacaactggtctt 3248  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 181 atccacagcccctgctcaattccagcatgtgtctagaggacagcagatacaactggtctt 240  
 KIAA0548 protein 60 Y P Q P L L N S S M C L E D S R Y N W S

Query: 3249 tcattcactgtccagcttgccaatgcaacggccacagtaaatgcatcaatcagagcatct 3308  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 241 tcattcactgtccagcttgccaatgcaacggccacagtaaatgcatcaatcagagcatct 300  
 KIAA0548 protein 80 F I H C P A C Q C N G H S K C I N Q S I

Query: 3309 gtgagaagtgtgagaacctgaccacaggcaagcactgcgagacctgcatatctggcttct 3368  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 301 gtgagaagtgtgagaacctgaccacaggcaagcactgcgagacctgcatatctggcttct 360  
 KIAA0548 protein 100 C E K C E N L T T G K H C E T C I S G F

Query: 3369 acggtgatcccaccaatggagggaatgtcagccatgcaagtgcaatgggcacgcgtctc 3428

Sbjct: 361 ||| acggtgatcccaccaatggagggaaatgtcagccatgcaagtgcaatgggcacgcgtctc 420  
 KIAA0548 protein 120 Y G D P T N G G K C Q P C K C N G H A S

Query: 3429 tgtgcaacaccaacacgggcaagtgtctctgcaccaccaagggcgtcaagggggacgagt 3488  
 Sbjct: 421 ||| tgtgcaacaccaacacgggcaagtgtctctgcaccaccaagggcgtcaagggggacgagt 480  
 KIAA0548 protein 140 L C N T N T G K C F C T T K G V K G D E

Query: 3489 gccagctatgtgaggtagaaaatcgataccaaggaaaccctctcagaggaacatgttatt 3548  
 Sbjct: 481 ||| gccagctatgtgaggtagaaaatcgataccaaggaaaccctctcagaggaacatgttatt 540  
 KIAA0548 protein 160 C Q L C E V E N R Y Q G N P L R G T C Y

Query: 3549 atactcttcttattgactatcagttcacctttagtctatcccaggaagatgatcgctatt 3608  
 Sbjct: 541 ||| atactcttcttattgactatcagttcacctttagtctatcccaggaagatgatcgctatt 600  
 KIAA0548 protein 180 Y T L L I D Y Q F T F S L S Q E D D R Y

Query: 3609 acacagctatcaattttgtggctactcctgacgaacaaaacagggatttggacatgttca 3668  
 Sbjct: 601 ||| acacagctatcaattttgtggctactcctgacgaacaaaacagggatttggacatgttca 660  
 KIAA0548 protein 200 Y T A I N F V A T P D E Q N R D L D M F

Query: 3669 tcaatgcctccaagaatttcaacctcaacatcacctgggctgccagtttctcagctggaa 3728  
 Sbjct: 661 ||| tcaatgcctccaagaatttcaacctcaacatcacctgggctgccagtttctcagctggaa 720  
 KIAA0548 protein 220 I N A S K N F N L N I T W A A S F S A G

Query: 3729 cccaggctggagaagagatgcctgttggttcaaaaaccaacattaaggagtacaaagata 3788  
 Sbjct: 721 ||| cccaggctggagaagagatgcctgttggttcaaaaaccaacattaaggagtacaaagata 780  
 KIAA0548 protein 240 T Q A G E E M P V V S K T N I K E Y K D

Query: 3789 gtttctctaatagagaagtttgattttcgcaaccacccaaatatcactttcttggtttatg 3848  
 Sbjct: 781 ||| gtttctctaatagagaagtttgattttcgcaaccacccaaatatcactttcttggtttatg 840  
 KIAA0548 protein 260 S F S N E K F D F R N H P N I T F F V Y

Query: 3849 tcagtaatttcacctggcccatcaaaattcagattgccttctctcagcacagcaatttta 3908  
 Sbjct: 841 ||| tcagtaatttcacctggcccatcaaaattcagattgccttctctcagcacagcaatttta 900  
 KIAA0548 protein 280 V S N F T W P I K I Q I A F S Q H S N F

Query: 3909 tggacctggtacagttcttcgtgactttcttcagttgtttcctctcttggctcctggtgg 3968  
 Sbjct: 901 ||| tggacctggtacagttcttcgtgactttcttcagttgtttcctctcttggctcctggtgg 960  
 KIAA0548 protein 300 M D L V Q F F V T F F S C F L S L L L V

Query: 3969 ctgctgtgggtttggaagatcaaacaaagtgtgtgggcctccagacgtagagagcaacttc 4028  
 Sbjct: 961 ||| ctgctgtgggtttggaagatcaaacaaagtgtgtgggcctccagacgtagagagcaacttc 1020  
 KIAA0548 protein 320 A A V V W K I K Q S C W A S R R R E Q L

Query: 4029 ttcgagagatgcaacagatggccagccgctccctttgcctctgtaaagtgcgccttgga 4088  
 |||||  
 Sbjct: 1021 ttcgagagatgcaacagatggccagccgctccctttgcctctgtaaagtgcgccttgga 1080  
 KIAA0548 protein 340 L R E M Q Q M A S R P F A S V N V A L E

Query: 4089 cagatgaggagcctcctgatcttattggggggagtataaagactgttcccaaaccattg 4148  
 |||||  
 Sbjct: 1081 cagatgaggagcctcctgatcttattggggggagtataaagactgttcccaaaccattg 1140  
 KIAA0548 protein 360 T D E E P P D L I G G S I K T V P K P I

Query: 4149 cactggagccgtgttttggcaacaaagccgctgtcctctctgtgtttgtgaggctccctc 4208  
 |||||  
 Sbjct: 1141 cactggagccgtgttttggcaacaaagccgctgtcctctctgtgtttgtgaggctccctc 1200  
 KIAA0548 protein 380 A L E P C F G N K A A V L S V F V R L P

Query: 4209 gaggcctgggtggcatccctcctcctgggcagtcaggctcttgctgtggccagcgccctgg 4268  
 |||||  
 Sbjct: 1201 gaggcctgggtggcatccctcctcctgggcagtcaggctcttgctgtggccagcgccctgg 1260  
 KIAA0548 protein 400 R G L G G I P P P G Q S G L A V A S A L

Query: 4269 tggacatttctcagcagatgccgatagtgtacaaggagaagtcaggagccgtgagaaacc 4328  
 |||||  
 Sbjct: 1261 tggacatttctcagcagatgccgatagtgtacaaggagaagtcaggagccgtgagaaacc 1320  
 KIAA0548 protein 420 V D I S Q Q M P I V Y K E K S G A V R N

Query: 4329 ggaagcagcagccccctgcacagcctgggacctgcatctga 4369  
 |||||  
 Sbjct: 1321 ggaagcagcagccccctgcacagcctgggacctgcatctga 1361  
 KIAA0548 protein 440 R K Q Q P P A Q P G T C I ^^^